RAW SEQUENCE LISTING   DATE: 03/04/2003
PATENT APPLICATION: US/09/105,117K   TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt
Output Set: N:\CRF4\03042003\I105117K.raw


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 3 <110> APPLICANT: Forschungszentrum Juelich GmbH; Marina Vrlijc et al.
 5 <120> TITLE OF INVENTION: Process for the microbial production of amino acids by
 6       boosted activity of export carriers
 8 <130> FILE REFERENCE: 1
10 <140> CURRENT APPLICATION NUMBER: US/09/105,117K
11 <141> CURRENT FILING DATE: 1998-06-17
12 <150> PRIOR APPLICATION NUMBER: PCT/DE96/02485
13 <151> PRIOR FILING DATE: 1996-12-18
14 <160> NUMBER OF SEQ ID: 5
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2374
20 <212> TYPE: DNA
21 <213> ORGANISM: Corynebacterium glutamicum
22 <220> FEATURE:
23 <221> NAME/KEY: gene
24 <222> LOCATION: CDS (1016)...(1726)
25 <223> OTHER INFORMATION: (LysE)
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32 gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180
34 gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240
36 ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300
38 cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360
40 acggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcatcgcag cccaatctag 420
42 tttcccatca accatgtagg catcccgcaa tgagggggtt gcaatggcca agtggcgcat 480
44 ggttccaagt tctactactt cacatcccgc cacgggatta gcttcacggg ttaccgctcc 540
46 taaaacatct ccacgccgca gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600
48 gagcgttgct ccaccccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660
50 cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttgcgc 720
52 tttagtttct gcttgcagca acaccatttt ccgcgctgct tgcacaagga cttcacccgc 780
54 ttcggttgct ttggccggtt gggtgcgcga taccaacact cgacccacgt gatgctcgag 840
56 agctttaacg cgctgactca ccgccgaggg ggaaatggaa agggctaagg aggcgccttc 900
59 gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960
61 atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg   1018
62                                                                Met
63                                                                  1
65 gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt   1066
66 Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
67               5                   10                  15
69 tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att   1114
70 Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile
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71         20                25                30
73 aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac   1162
74 Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
75         35                40                45
77 gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat   1210
78 Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
79 50                55                60                65
81 gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac   1258
82 ·Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr
83                70                75                80
85 ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag   1306
86 Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
87                85                90                95   .
89 gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat   1354
90 Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
91         100               105               110
93 gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg   1402
94 Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
95         115               120               125
97 gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc.  1450
98 Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
99 130               135               140               145
101 atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg  1498
102 Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
103               150               155               160
105 gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc  1546
106 Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
107               165               170               175
109 gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg  1594
110 Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
111         180               185               190
113 ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc  1642
114 Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
115         195               200               205
117 agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg  1690
118 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
119 210               215               220               225
121 acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg       1736
122 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
123    ·              230               235
125 ttttggaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtgggaa atctcatcga 1796
127 tcgcctccaa ctcggcgtca gaaaactcca agttgttgag tgaatcaagg ctgttgtcca 1856
129 gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916
131 cttgctcgcg cagcacccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976
133 cgatgtcatt gagcttgcgg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036
135 gggacttacc ctggctggcg cgggaaccct ctggaattcc atcgagatat ttgtccgtga 2096
137 gcaggccctg cgcaagtggt gagaaagcaa tgacgccaag accattgttg cagctgact  2156
139 gcaacaagtt ctcaccgtca tcgcccggtt cctccaccca acgattaatg atggaatagc 2216
141 ttggctgatg aatcagaagc gggcagccct cctccgccat gaactcagcc gcctccgctg 2276
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Input Set : A:\Seq_listing_US_korrigiert130203.txt
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143 tgagctctgg accgtaggaa gaaatacccca cgtaaagagc ctttccagac gcaacaatgt 2336
145 cacgcaatgc gtacatggtt tcttccaaag gagtatct                        2374
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 236
152 <212> TYPE: PRT
153 <213> ORGANISM: Corynebacterium glutamicum
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155 <223> OTHER INFORMATION: (LysE)
157 <400> SEQUENCE: 2
158 Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
159  1               5                  10                  15
161 Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
162              20                  25                  30
164 Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
165          35                  40                  45
167 Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
168      50                  55                  60
170 Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
171  65                  70                  75                  80
173 Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
174              85                  90                  95
176 Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
177          100                 105                 110
179 Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
180          115                 120                 125
182 Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
183      130                 135                 140
185 Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
186 145                 150                 155                 160
188 Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
189              165                 170                 175
191 Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
192          180                 185                 190
194 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
195          195                 200                 205
197 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
198      210                 215                 220
200 Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
201 225                 230                 235
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 2374
209 <212> TYPE: DNA
210 <213> ORGANISM: Corynebacterium glutamicum
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212 <221> NAME/KEY: unsure
213 <222> LOCATION: CDS (2)..(652)
214 <223> OTHER INFORMATION: orf3
215         (complement to SEQ ID No. 1)
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W--> 216 <220> FEATURE:

RAW SEQUENCE LISTING   DATE: 03/04/2003
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Input Set : **A:\Seq_listing_US_korrigiert130203.txt**
Output Set: **N:\CRF4\03042003\I105117K.raw**

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218 <222> LOCATION: CDS (1421)..(2293)
219 <223> OTHER INFORMATION: LysG
221 <400> SEQUENCE: 3
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224   1               5                  10                  15
226 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc  97
227 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
228             20                  25                  30
230 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg  145
231 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
232         35                  40                  45
234 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg  193
235 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
236     50                  55                  60
238 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt  241
239 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
240 65                  70                  75                  80
242 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa  289
243 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
244             85                  90                  95
246 tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc  337
247 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
248         100                 105                 110
250 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag  385
251 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
252         115                 120                 125
254 ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg  433
255 Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
256     130                 135                 140
258 ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg  481
259 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
260 145                 150                 155                 160
262 acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc  529
263 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
264             165                 170                 175
266 ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg  577
267 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
268         180                 185                 190
270 atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc  625
271 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
272         195                 200                 205
274 acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat  672
275 Thr Asp Ser Lys Thr Arg Glu Asn
276     210                 215
278 ggccaatgcg gtcatcacaa ctgccacgac gacgttgatc cagcgccaca ccttggggct  732
280 ggacagcggg cgtgacaatg ctgctgcgcc gaaacccacc agcgggaacc agatcaggct  792
282 tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac  852
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       284 gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat 912
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       288 ccggttgcgc gtgtcagtgg ccaccgccga accgcccaaa ggcgtgtcat cgggcacggt 1032
       290 tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc 1092
       292 tgccatgacg gcaaaccata acaggtaagc gatgccaccc cagcgcataa tatcgagcac 1152
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       296 gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt 1272
       298 aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccca aaagcagacc 1332
       300 tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392
       302 ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act    1444
       303                                 Met Asn Pro Ile Gln Leu Asp Thr
W--> 304                                             220                 225
       306 ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc   1492
       307 Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
W--> 308                 230                 235                 240
       310 ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag   1540
       311 Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
W--> 312             245                 250                 255
       314 cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca   1588
       315 His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
W--> 316             260                 265                 270
       318 acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg   1636
       319 Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
W--> 320         275                 280                 285
       322 ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc   1684
       323 Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
W--> 324 290                 295                 300                 305
       326 ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct   1732
       327 Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
W--> 328                 310                 315                 320
       330 ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg   1780
       331 Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
W--> 332             325                 330                 335
       334 cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat   1828
       335 Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
W--> 336             340                 345                 350
       338 gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa   1876
       339 Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
W--> 340         355                 360                 365
       342 gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca   1924
       343 Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
W--> 344 370                 375                 380                 385
       346 ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg   1972
       347 Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
W--> 348             390                 395                 400
       350 ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg   2020
       351 Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
W--> 352             405                 410                 415
       354 gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc   2068
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/04/2003
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<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY   DATE: 03/04/2003
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L:22  M:283 W: Missing Blank Line separator, <220> field identifier
L:154 M:283 W: Missing Blank Line separator, <220> field identifier
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